

AMENDMENTS TO THE SPECIFICATION

Insert the attached sheet entitled "Abstract" after the claims as page number 50.

Insert the Sequence Listing as separately numbered pages 1 - 86 after the abstract.

Replace the paragraph beginning at page 6, line 4 with the following amended paragraph:

Figure 3. (a) The The amino acid sequence of IL-6R extracellular domain (SEQ ID No: 83), showing the CBD comprising domain D2 (residues 92 to 195) and domain D3 (residues 196 to 297). The position of β -sheet structures are indicated by #. The position of loops in the cytokine binding region are shown by * and marked L1 to L7. The Pro94, Pro95, Cys102, Cys103, Trp115, Cys146, Cys157, Pro199, Pro200, Trp219, Arg274, Trp284, Ser285, Trp287 and Ser288 residues are all conserved in known CBDs. The Leu100, Leu108, Val111, Ala127, Leu129, Val131, Leu159, Tyr169, Val171, Met173, Val175, Phe189, Gly191, Ile194, Leu195, Pro197, Ile203, Val205, Leu215, Val217, Leu232, Phe234, Leu236, Tyr238, Phe246, Trp249, Ile260, Ala263, Val271, Leu273, and Glu286 residues are mainly conserved hydrophobic residues in known CBDs. The Pro98, Pro117, Trp225, Cys258, His269, Ala291 and Gly293 are, in the majority, conserved residues in all known CBDs.

Replace the paragraph beginning at page 6, line 16 with the following amended paragraph:

Figure 3(b) Figure 3A depicts the sequence alignment of the CBDs from IL-6R, IL-11R, PRLR and GCSR. Loops L1 to L7 are outlined by boxes.

Replace the paragraph beginning at page 6, line 23 with the following amended paragraph:

Figure 5. Comparison of the sequences of CBDs from a number of known 77 known genes (SEQ ID Nos:1-82). Figure 5A compares the sequences in the "first" FnIII domain, containing loops 1 to 4, and Figure 5B the sequences in the "second" FnIII domain, containing the loops 5-7. Conserved residues as described in Example 3 for the IL-6 receptor are aligned according to their sequence homologies. For example the hydrophobic residues, the cysteine residues (C) and in some cases two prolines side by side (PP) are aligned. The location of the 7 binding loops is indicated by the double-headed arrows..

Replace the paragraph beginning at page 35, line 16 with the following amended paragraph:

The partial DNA sequence of IL-6R D3 (loops 6 and 7 in bold and boxed, and Cys258 in bold) is shown below as sequence (a). The corresponding partial DNA sequence of the D3 library clone, showing changes in loop 6 and at Cys258 (mutated to Ser) shown as sequence (b).

(a) R S K T F T T W **M V K D L** Q H H C V I H D A W S G L R H
(b) R S K T F T T W **A Q S R W** Q H H S V I H D A W S G L R H

(a) V V Q L R A **Q E E F G Q G** E W S E W (SEQ ID No:84)
(b) V V Q L R A **Q E E F G Q G** E W S E W (SEQ ID No:85)

Replace the paragraph beginning at page 35, line 32 (and ending at page 36, line 2) with the following amended paragraph:

The partial DNA sequence of IL-6R D3 (loops 6 and 7 in bold and boxed, and Cys258 in bold) is shown below as sequence (c). The corresponding partial DNA

sequence of the D3 library clone, showing changes in loops 6 and 7 and at Cys258 (mutated to Ser) shown as sequence (d).

(c) R S K T F T T W **M V K D L** Q H H C V I H D A W S G L R H
(d) R S K T F T T W **S R Q N D** Q H H S V I H D A W S G L R H

(c) V V Q L R A **Q E E F G Q G** E W S E W (SEQ ID No:86)
(d) V V Q L R A **R N E V R V G** E W S E W (SEQ ID No:87)

Replace the paragraph beginning at page 37, line 3 with the following amended paragraph:

The CBD of human prolactin receptor has the following amino acid sequence **(SEQ ID No:21)**:

24	GQLPPGK PEIFKCR SPN KETFT CWWRP GTDGLPTNY	
	L1	
61	SLT YHREGET LMHECPDYIT GGPNSCH FGK QYTSMWRTYI	
	L2	L3
101	MMVNATNQMG SSFSDE LYVD V TYIVQPDPP LELAVEVKQP	
	L4	
141	EDRKPYLWIK WSPPTL IDLK TGWFT LLYEI RLKPEKAAEW	
	L5	
181	EIHFA GQQTE F KILSLHPGQ KYLVQVR CKP DHGY WSAWSP	
	L6	L7
221	ATFIQIPSD 229	

The first FnIII-like domain is defined by amino acids Glu24 to Val125 and the second Fn-III like domain by Gln126 to Asp229. Loops L1 to L7 are indicated as boxed residues on the above sequence.

Replace the paragraph beginning at page 38, line 3 with the following amended paragraph:

The CBD of IL-11R has the following amino acid sequence (SEQ ID No:27):

111 YPPARPVVSC QAADYENFSC TWSPSQISGL PTRYLTYSRK
L1
151 KTVLGADSQR RSPPSTGPWPC PQDPLGAARC VVHGAEFWSQ
L2 L3
191 YRINVTEVNP LGASTRLLDV SLQSILRPDP PQGLRVESVP
L4
231 GYPRRLRASW TYPASWPCQP HFLLKFRLQY RPAQHPAWST
L5
271 VEPAGLEEVI TDAVAGLPHA VRVSARDFLD AGTWSTWSPE
L6 L7
321 AWGTPSTGT 329
321 AWGTPSTG 328

The first FnIII-like domain is defined by amino acids 112-214 and the second FnIII-like domain by amino acids 218-318. Loops L1 to L7 are indicated as boxed residues on the above sequence.

Replace the paragraph beginning at page 38, line 31 with the following amended paragraph:

The first FnIII-like domain derived from the CBD of prolactin receptor is defined by residues 24-125 ~~[IS THIS CORRECT see Ex-9 questions]~~ as in Example 9.

Replace the paragraph beginning at page 38, line 34 (and ending on page 39, line 8) with the following amended paragraph:

The CBD of GSCFR has the following amino acid sequence (SEQ ID No:2):

121 YPPAIPHNL_S CL_{MNL}TTSSL I_CQWE_PGPET HLPT_SFTLKS
L1

161 F_KSRGN_CQT_Q GDS_ILD_CVPK DGQSHCC_IP_R KH_{LLL}YQ_NMG
L2 L3

201 I_WVQAENALG TSMSPQL_CI_D PMD_VV_KLEPP MLRTMDPSPE
L4

241 AAPPQAGCLQ LCWE_PWQ_PG_L H_INQKCE_LR_H KPQRGEASWA
L5

281 LVGPLP_LE_AL Q_YELCGLLPA TAYTLQIRC_I RWPLP_GHWS_D
L6 L7

321 WSPSLELRTT ERA 333

Loops L1 to L7 of the CBD of GCSFR are indicated as boxed residues on the above sequence. The second region of the CBD of GCSFR is defined by residues 237-330.